AMENDMENTS TO THE DRAWINGS

Replacement Figures 15, 16 and 17 are now provided.

REMARKS

Claims 1-26 were originally filed in the present application. In the Restriction Requirement Response mailed July 27, 2004, the Applicants elected, without traverse, to prosecute the claims of Group I (Claims 1-10), and the species of SEQ ID NO: 1. Applicants also canceled claims 11-16 in order to further their business interests and the prosecution of the present application, yet without acquiescing to the Examiner's arguments, and while preserving the right to prosecute the canceled (or similar) claims in the future. Additionally, the Applicants canceled Claims 1-10, amended Claims 17-20, and provided new Claims 27-35.

In an Office Action mailed December 16, 2004, the Examiner made several objections to the Specification, and rejected Claims 17-35. Each objection and rejection is discussed below.

I. Objections To The Specification

The Examiner made numerous objections to the Specification. Office Action, pages 2-3. The Applicants now provide amendments to the Specification per the requests of the Examiner. No new matter was added in the amendments.

II. Objection To The Claims

The Examiner states, "Applicant is advised that should claims 17, 20, 21, 22, 23, 24 and 25, be found allowable, claims 19, 27, 30, 31, 32, 33, 34 and 35 will be objected to under 37 C.F.R. 1.75 as being a substantial duplicate thereof." Office Action, page 4. The Applicants now cancel Claims 19, 27, 30, 31, 32, 33, 34 and 35.

III. Rejection To Claims 17-35 Under 35 U.S.C. §112(1), Written Description

Claims 17-35 are rejected under 35 U.S.C. §112(1) as failing to comply with the written description requirement. In particular, the Examiner alleges, "The specification does not describe any variants of SEQ ID No.1 with at least 80%, 90%, or 95% sequence identity with SEQ ID No. 1...The specification does not correlate the function of directing gene expression to a greater or equal extent in non-seed tissues versus seed tissues with the sequences of SEQ ID No. 1 or any variant thereof. Given the breadth of

the claims encompassing nucleotide sequences that are at least 80% identical to SEQ ID No. 1, and the lack of written description as discussed above, the specification fails to provide an adequate written description of the multitude of polynucleotides encompassed by the claims." Office Action, pages 6-7.

The Examiner's rejection is inconsistent with the USPTO's own guidelines for examination under the written description requirement. Recent Federal Circuit precedent establishes that determinations of whether the written description requirement have been met should be consistent with both Federal Circuit precedent and the written description guidelines. *Enzo Biochem, Inc. v. Gen-Probe, Incorporated*, 323 F.3d 956 (Fed. Cir. 2002).

Contrary to the Examiner's assertions, the Specification does indeed show that the Inventors had possession of the claimed invention. For example, the Inventors constructed a cDNA library from *Arabidopsis thaliana* seed collections; sequenced the cDNAs; cloned the cDNAs in expression vectors; matched the cDNAs against existing libraries; generated a list of ESTs; amplified, arrayed and hybridization analyzed the ESTs using RNA extracted from *Arabidopsis thaliana* plants; performed seed-specific promoter analysis by comparing ESTs using BLAST against *Arabidopsis* genomic sequences; selected for PCR amplification the promoter regions approximately 1kb upstream of ATG; fused the promoter regions to promoterless β-GUS expression vectors; transformed *Arabidopsis thaliana* plant tissues; and analyzed promoter activity by histochemistry, time of expression, and quantification of GUS expression levels as a function of gene copy number and chromosomal insertion position effects (Specification, Examples I, II and III). The Examiner is further directed to the Specification at, for example, page 50, lines 7-21:

> Accordingly, in some embodiments, the present invention provides methods by which genomic sequences under control of the promoter regions of the present invention (as for example, genes 1-20 as described in Table 2, as shown in Figure 18) are used to identify additional homologous genomic sequences, preferably from other plants; the promoter regions of these homologous genomic sequences are then identified and isolated as described previously. Thus, in some aspects of the present invention, an at least partial genomic sequence of a plant is analyzed for

> sequences which are homologous to the *Arabidipsis* sequences which are identified as being specifically expressed in seeds (for example, those Arabidopsis sequences listed in Table 2, as shown in Figure 18). For example, BLAST searches (Altshul *et al.*, Nucleic Acids Res. 25:3389-3402 (1997)) may be utilized to search for nucleic acids having homology (for example, greater than 60%, 70%, 80%, or 90%) to the *Arabidopsis* sequences identified as expressed seed-specifically. Once homologous seed-specific genetic sequences are identified and isolated, they can be used to isolate promoter sequences as described above.

Thus, it is clear that the Inventor's contemplated and were in possession of the claimed invention.

The Applicants refer the Examiner to Example 14 of the USPTO's "Synopsis of Application of Written Description Guidelines" (pertinent pages attached at Appendix B). The claim of Example 14 recites a protein having SEQ ID NO:3 and variants thereof that are at least 95% identical to SEQ ID NO:3 and catalyze the reaction of A->B. The disclosure of Example 14 provides a single species (SEQ ID NO:3) that has actually been reduced to practice, and describes an assay for identifying the variants having the desired catalytic activity. The analysis considers (1) whether the members of genus vary substantially from each other; and (2) whether the disclosed species is representative of the members of the genus; in order to determine whether one of skill in the art would determine if the applicant was in possession of the necessary common attributes possessed by the members of the genus.

For Example 14, it was determined that the member species did not substantially vary since the variants have 95% identity or greater to the reference sequence, and also possess the catalytic activity. It was also determined that the disclosed species was representative since all members must have at least 95% structural identity to SEQ ID NO:3. The analysis determined that one of skill in the art would conclude that the applicant was in possession of the necessary common attributes possessed by the members of the genus, and therefore the disclosure in this Example meets the written description requirement.

The Applicants submit that Claims 17-35 can be analyzed in a similar manner to that provided in Example 14. First, the sequence variants described in Claims 17-35 do not substantially vary as members of a genus since they all have at least 80% identity to SEQ ID NO:1 and, per limitation of the claims, must possess the same seed-specific promoter activity. Second, SEQ ID NO: 1 is a representative species of the genus since all polypeptides must have at least 80% identity to this sequence. Third, as with Example 14, a type of detection is provided for detecting for identifying variants with the desired promoter activity. Therefore, one of skill in the art would conclude that the Inventors were in possession of the necessary common attributes possessed by the members of the genus, and therefore the instant specification meets the written description requirement for these claims. The Applicants respectfully requests that the Examiner reconsider and withdraw the rejections of the claims on the basis of the 35 U.S.C. § 112, first paragraph, written description requirement.

IV. Rejection Of Claims 17-35 Under 35 U.S.C. §112(1), Enablement

The Examiner rejected Claims 17-35 under 35 U.S.C. § 112, first paragraph as not being enabled by the Specification. In particular, the Examiner alleged, "[T]he specification, while being enabling for the promoter sequence of SEQ ID NOs. 1, does not reasonably provide enablement for variants thereof that are at least 80% identical to SEQ ID No. 1 that retain promoter activity...The claimed invention is not supported by an enabling disclosure taking into account the *Wands* factors...Given the breadth of the claims encompassing SEQ ID No. 1 and variants thereof having at least 80%, 90%, or 95% sequence identity with SEQ ID No. 1, the lack of guidance of the specification as discussed above, the unpredictability of the art, and the plethora of possible permutations and combinations to which SEQ ID No. 1 and variants thereof can be subjected in order to determine how the sequences might be changed without affecting promoter activity, it would require undue experimentation by one skilled in the art to make and use the invention as claimed." Examiner Action, pages 8-10.

The rejection is in error because the Examiner failed to establish a *prima facie* case of non-enablement. The standard to be applied in assessing enablement is whether the experimentation needed to practice the claimed invention is undue or unreasonable.

See TRAINING MATERIALS FOR EXAMINING PATENT APPLICATIONS WITH RESPECT TO 35 U.S.C. SECTION 112, FIRST PARAGRAPH-ENABLEMENT CHEMICAL/BIOTECHNICAL APPLICATIONS, *citing In re Wands*, 8 USPQ2d 1400, 1404 (Fed. Cir. 1988). When applying this standard, the burden is on the Examiner to make a *prima facie* case of non-enablement that is well grounded in scientific reasoning or evidence. *See In re Wright*, 27 USPQ2d 1510 (Fed. Cir. 1993); *See also* MPEP §706.03 and §2164.04. This is because without a reason to doubt the truth of the statements made in the patent application, the application must be considered enabling (*Wright,* 27 USPQ2d at 1513).

Applicant respectfully submits that proper analysis applying the *Wands* factors supports the conclusion that the claims are enabled. As described in the MPEP §2164.01(a), the Wands factors include: a) The breadth of the claims; b) The nature of the invention; c) The state of the prior art; d) The level of ordinary skill in the art; e) The level of predictability in the art; f) The amount of direction provided by the inventor; g) The existence of working examples; and h) The quantity of experimentation needed to make or use the invention based on the content of the disclosure. *See also*, *In re Wands*, 858 F.2d 731, 737 (Fed. Cir. 1988).

As noted in the MPEP:

> It is improper to conclude that a disclosure is not enabling based on an analysis of only one of the above factors while ignoring one or more of the others. The examiner's analysis must consider all of the evidence related to each of these factors, and any conclusion of non-enablement must be based on the evidence as a whole.

MPEP §2164.01(a)(citing *In re Wands*, 858 F.2d 731, 740 (Fed. Cir. 1988)(emphasis added)).

Applicant respectfully submits that the Examiner's analysis, discussed in more detail below, completely fails to properly address the *Wands* factors. As noted in the MPEP, the analysis must be of the disclosure. Indeed, because the cDNA of, for example, SEQ ID NO:1 is provided in the specification, it is straightforward to determine what variations of the nucleotide sequences falls within the 80% sequence identity limitation recited in the claims while maintaining the property of being a seed-specific

promoter. Such variations are described in the specification on, for example, page 50, lines 7-21. These additional molecules can be generated according to methods described in the specification and methods well known in the art.

This evidence establishes that the specification teaches in detail how to: 1) make variants of SEQ ID NO: 1; 2) calculate the percent identity between SEQ ID NO: 1 and a variant sequence; and 3) test the variant sequence to determine if it possesses seed-specific promoting properties (see, e.g., Example III).

Application of the *Wands* factors to these facts supports the conclusion that the claims are enabled. First, the present invention is in the field of molecular biology. The *Wands* court has already held that the level of skill in this art is high. *Wands*, 858 F.2d at 740. Second, as the citations to the specification above prove, the specification provides considerable guidance and direction for producing the claimed nucleic acid sequences. Third, as in *Wands*, the methods of making the claimed nucleic acid sequences and screening for activity are known in the art and described in the specification at the cited passages. *Id.* Fourth, as admitted by the Examiner, SEQ ID NO: 1 is a working example for a promoter sequence. Fifth, given the extensive guidance given in the specification (cited above) and the high level of skill in the art, the experimentation involved to produce other sequences within the scope of the claims is well within the skill of those in the art. As held by the *Wands* court: "The test is not merely quantitative since as considerable amount of experimentation is permissible, if it is merely routine, or if the specification in question provides a reasonable amount of guidance with respect to the direction in which the experiment should proceed. *Id.* at 737.

Turning to the claims at issue, as part of the enablement analysis, the scope of the claims must be considered. MPEP § 2164.04. Independent Claims 17 and 18 are directed to a method for producing a product or protein of interest in a plant seed comprising providing a transgenic plant comprising a nucleic acid sequence encoding the product or protein of interest operably linked to a promoter region with seed-specific promoter activity, wherein the promoter is selected from the group consisting of SEQ ID NO: 1 and variants thereof that are at least 80% identical to SEQ ID NO: 1, and growing the plant. Claim 20 is directed to an isolated DNA molecule comprising a seed-specific promoter region selected from the group consisting of SEQ ID NO: 1 and variants thereof

that are at least 80% identical to SEQ ID NO: 1, and a heterologous gene operably linked to the promoter region.

As described above, given the high level of skill in the art, extensive guidance in the specification, methods known in the art, the production of and isolation of the claimed nucleic acid sequences which are greater than 80% identical to SEQ ID NO: 1 while retaining seed-specific promoter activity does not require undue experimentation. Thus, Applicant respectfully submits that Claims 17-35 are enabled.

V. Rejection To Claims 17-35 Under 35 U.S.C. §112(2)

Claims 17-35 are rejected under 35 U.S.C. §112(2). In particular, the Examiner alleges, "Claim 17-35 rejected under 35 U.S.C. §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention...Claim 19 recites the limitation 'the product of interest' in line 4. There is insufficient basis for this limitation in the claim...Claims 17-20 and 27 recite 'seed specific'. The definitions of 'tissue specific' on page 2, lines 4-8 and 'seed specific' on page 25, lines 4-10 are inconsistent. The definition on page 25 encompasses promoters that do not direct gene expression to a greater extent in seed tissues versus non-seed tissues. The definition on page 25 encompasses promoters that direct expression in seed, but also include those that direct equal or higher levels of gene expression in other tissues. It is not clear what is specifically meant by 'seed specific' as recited." Office Action, pages 10-11.

Regarding the definition of "seed specific promoter," the Applicants respectfully disagree. The term "seed-specific promoter" is defined within the Specification. Whether the Examiner considers the definition of "tissue specific" and "seed-specific" to be inconsistent is irrelevant. Regarding Claims 17-35, the Examiner is directed to the definition of seed-specific promoter on page 25, lines 4-10.

Regarding Claim 19, the Applicants now cancel Claim 19. The Applicants reserve the right to prosecute the original Claim 19 or similar claims in the future.

VI. Rejection Of Claims 20, 27, 28 and 29 Under 35 U.S.C. §102(b)

Claims 20, 27, 28 and 29 are rejected under 35 U.S.C. §102(b). In particular, the Examiner alleges, "Claims 20, 27, 28 and 29 are rejected under 35 U.S.C. §102(b) as being anticipated by EMBL database posting: accession number AL021749, *Arabidopsis* Thaliana DNA chromosome 4, BAC clone F2009, publication date: August 3, 1999, or by EMBL database posting: accession number AL161573, *Arabidopsis thaliana* DNA chromosome 4, Contig fragment No. 69, publication date: March 16, 2000. Claims 20, 27, 28 and 29 recite an isolated DNA molecule comprising the promoter region, wherein the promoter region is a seed-specific promoter and is selected from the group consisting of SEQ ID No. 1 and variants thereof that are at least 80%, 90% and 95% identical to SEQ ID No.1. The EMBL database sequence postings of accession numbers AL021749 and AL161573 are chromosome 4 genomic clones derived from *Arabidopsis thaliana* comprising SEQ ID No. 1." Office Action, page 11.

The Applicants respectfully disagree. However, in order to expedite prosecution, Claim 20 is amended such that the isolated DNA molecule further comprises a heterologous gene operably linked to the plant promoter. The prior art does not teach or describe an isolated DNA molecule comprising a) a seed-specific plant promoter region selected from the group consisting of SEQ ID NO: 1 and variants thereof that are at least 80% identical to SEQ ID NO: 1, and b) a heterologous gene operably linked to the plant promoter region.

CONCLUSION

All grounds of rejection of the Office Action of December 16, 2004 have been addressed and reconsideration of the application is respectfully requested. It is respectfully submitted that Applicant's new claims should be passed into allowance. Should the Examiner believe that a telephone interview would aid in the prosecution of this application Applicant encourages the Examiner to call the undersigned collect at (608) 218-6900.

Dated: 6/16/05

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